

Ex Search notes
for Screen

RESULT 1

US-09-156-580-14

; Sequence 14, Application US/09156580A
; Patent No. 6215043
; GENERAL INFORMATION:
; APPLICANT: Takatsuji, Hiroshi
; APPLICANT: Nakagawa, Hitoshi
; APPLICANT: Director General of National Institute of Agrobiological
; APPLICANT: Resources, Ministry of Agriculture, Forestry and Fisheries
; TITLE OF INVENTION: Method for Shortening Internode of Inflorescence by
; TITLE OF INVENTION: Introducing Gene for Petunia Transcription Factor PetSPL2
; FILE REFERENCE: 085761-000400US
; CURRENT APPLICATION NUMBER: US/09/156,580A
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: JP 10-224852
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SUPERMAN
; OTHER INFORMATION: C-terminal hydrophobic region
US-09-156-580-14

Query Match 90.5%; Score 38; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLELRL 9
|||
Db 23 DLDLELRL 30

102 e Clns 17, 18

RESULT 1

S60325

transcription factor SUPERMAN - Arabidopsis thaliana

N;Alternate names: CCHH zinc finger protein

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 06-Sep-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C;Accession: S60325

→ R;Sakai, H.; Medrano, L.J.; Meyerowitz, E.M.

Nature 378, 199-203, 1995

A;Title: Role of SUPERMAN in maintaining Arabidopsis floral whorl boundaries.

A;Reference number: S60325; MUID:96069740; PMID:7477325

A;Accession: S60325

A;Molecule type: mRNA

A;Residues: 1-204 <SAK>

A;Cross-references: UNIPROT:Q38895; UNIPARC:UPI000000A019D; EMBL:U38946;

NID:g1079668; PIDN:AAC49116.1; PID:g1079669

A;Note: DNA sequencing was also done

C;Genetics:

A;Gene: SUP

C;Keywords: DNA binding; leucine zipper; nucleus; transcription factor;
transcription regulation; zinc finger

Query Match 90.5%; Score 38; DB 2; Length 204;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLELRL 9

|||||||

Db 194 DLDLELRL 201

1026 cl 17, 18

Q9LTD6_ARATH

ID Q9LTD6_ARATH PRELIMINARY; PRT; 172 AA.
AC Q9LTD6;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 30.
DE Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K14B15.
GN OrderedLocusNames=At3g23140;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20277480; PubMed=10819329; DOI=10.1093/dnares/7.2.131;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB025608; BAA95725.1; -; Genomic_DNA.
DR HSSP; Q38895; 1NJQ.
DR TAIR; At3g23140; -.
DR GO; GO:0045449; P:regulation of transcription; TAS.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 172 AA; 18801 MW; 22836292963CF293 CRC64;

Query Match 90.7%; Score 39; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLRL 9
|||
Db 159 DLDLRL 166

↑

102 b

US-11-435-388-836

; Sequence 836, Application US/11435388
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert A
; APPLICANT: RATCLIFFE, Oliver J
; APPLICANT: CANALES, Roger D
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; APPLICANT: MORRISON, Tracy A
; APPLICANT: KEDDIE, James S
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: CENTURY, Karen S
; APPLICANT: ADAM, Luc
; APPLICANT: ZHANG, James Z
; APPLICANT: HEMPEL, Frederick D
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS
; FILE REFERENCE: 514442005421
; CURRENT APPLICATION NUMBER: US/11/435,388
; CURRENT FILING DATE: 2006-05-15
; PRIOR APPLICATION NUMBER: WO PCT/US2004/037584
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/714,887
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/527,658
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 60/542,928
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: US 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/533,029
; PRIOR FILING DATE: 2000-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1018
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 836
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G359 polypeptide
US-11-435-388-836

Query Match 83.3%; Score 35; DB 7; Length 204;
Best Local Similarity 87.5%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLDLQLRL 9
|||:|
Db 194 DLDLELRL 201

RESULT 1

S60325

transcription factor SUPERMAN - Arabidopsis thaliana

N;Alternate names: CCHH zinc finger protein

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 06-Sep-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C;Accession: S60325

R;Sakai, H.; Medrano, L.J.; Meyerowitz, E.M.

Nature 378, 199-203, 1995

A;Title: Role of SUPERMAN in maintaining Arabidopsis floral whorl boundaries.

A;Reference number: S60325; MUID:96069740; PMID:7477325

A;Accession: S60325

A;Molecule type: mRNA

A;Residues: 1-204 <SAK>

A;Cross-references: UNIPROT:Q38895; UNIPARC:UPI00000A019D; EMBL:U38946;

NID:g1079668; PIDN:AAC49116.1; PID:g1079669

A;Note: DNA sequencing was also done

C;Genetics:

A;Gene: SUP

C;Keywords: DNA binding; leucine zipper; nucleus; transcription factor;
transcription regulation; zinc finger

Query Match 83.3%; Score 35; DB 2; Length 204;

Best Local Similarity 87.5%; Pred. No. 9.5;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLQLRL 9

||||:|||

Db 194 DLDLELRL 201

RESULT 2

T02540

probable C2H2-type zinc finger protein At2g37740 [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein F13M22.24

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C;Accession: T02540; E84796

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.

submitted to the EMBL Data Library, June 1998

A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.

A;Reference number: Z14677

A;Accession: T02540

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-304 <ROU>

A;Cross-references: UNIPROT:O80942; UNIPARC:UPI000000AB7CB; EMBL:AC004684;

NID:g3236234; PID:g3236256

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84796

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-304 <STO>

A;Cross-references: UNIPARC:UPI000000AB7CB; GB:AE002093; NID:g3236256;

PIDN:AAC23644.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g37740; F13M22.24

A;Map position: 2

Query Match 83.3%; Score 35; DB 2; Length 304;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLQLRL 9
|||:|
Db 289 DLDLELRL 296

RESULT 1

US-09-156-580-14

; Sequence 14, Application US/09156580A
; Patent No. 6215043
; GENERAL INFORMATION:
; APPLICANT: Takatsuji, Hiroshi
; APPLICANT: Nakagawa, Hitoshi
; APPLICANT: Director General of National Institute of Agrobiological
; APPLICANT: Resources, Ministry of Agriculture, Forestry and Fisheries
; TITLE OF INVENTION: Method for Shortening Internode of Inflorescence by
; TITLE OF INVENTION: Introducing Gene for Petunia Transcription Factor PetSPL2
; FILE REFERENCE: 085761-000400US
; CURRENT APPLICATION NUMBER: US/09/156,580A
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: JP 10-224852
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SUPERMAN
; OTHER INFORMATION: C-terminal hydrophobic region

US-09-156-580-14

Query Match 83.3%; Score 35; DB 2; Length 33;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLDLQLRL 9
|||:|
Db 23 DLDLELRL 30

RESULT 4

US-09-156-579C-16

; Sequence 16, Application US/09156579C

; Patent No. 6297429

; GENERAL INFORMATION:

; APPLICANT: Takatsuji, Hiroshi

; APPLICANT: Nakagawa, Hitoshi

; APPLICANT: Director General of National Institute of Agrobiological Resources,

; APPLICANT: Ministry of Agriculture, Forestry and Fisheries

; TITLE OF INVENTION: Gene for Transcription Factor Capable of Altering

; TITLE OF INVENTION: Characters of a Plant and Use Thereof

; FILE REFERENCE: 085761-000300US

; CURRENT APPLICATION NUMBER: US/09/156,579C

; CURRENT FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: JP 10-065921

; PRIOR FILING DATE: 1998-03-16

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 33

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:C-terminal

; OTHER INFORMATION: hydrophobic region of SUPERMAN

US-09-156-579C-16

Query Match 83.3%; Score 35; DB 2; Length 33;

Best Local Similarity 87.5%; Pred. No. 2.7;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLQLRL 9

||||:||||

Db 23 DLDLELRL 30

RESULT 11

US-09-156-580-2

; Sequence 2, Application US/09156580A

; Patent No. 6215043

; GENERAL INFORMATION:

; APPLICANT: Takatsuji, Hiroshi

; APPLICANT: Nakagawa, Hitoshi

; APPLICANT: Director General of National Institute of Agrobiological

; APPLICANT: Resources, Ministry of Agriculture, Forestry and Fisheries

; TITLE OF INVENTION: Method for Shortening Internode of Inflorescence by

; TITLE OF INVENTION: Introducing Gene for Petunia Transcription Factor PetSPL2

; FILE REFERENCE: 085761-000400US

; CURRENT APPLICATION NUMBER: US/09/156,580A

; CURRENT FILING DATE: 1998-09-18

; EARLIER APPLICATION NUMBER: JP 10-224852

; EARLIER FILING DATE: 1998-08-07

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 206

; TYPE: PRT

; ORGANISM: Petunia sp.

US-09-156-580-2

Query Match 83.3%; Score 35; DB 2; Length 206;

Best Local Similarity 87.5%; Pred. No. 20;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLQLRL 9

||||:|||

Db 196 DLDLELRL 203

US-10-278-173-30
 ; Sequence 30, Application US/10278173
 ; Publication No. US20030061637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Broun, Pierre
 ; APPLICANT: Riechmann, Jose-Luis
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Zhang, James
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Pilgrim, Marsha
 ; APPLICANT: Keddie, James
 ; APPLICANT: Heard, Jacqueline
 ; APPLICANT: Reuber, Lynne
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Adam, Luc
 ; APPLICANT: Samaha, Raymond
 ; TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
 ; FILE REFERENCE: MBI-009
 ; CURRENT APPLICATION NUMBER: US/10/278,173
 ; CURRENT FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US/09/533,392
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/125,814
 ; PRIOR FILING DATE: 1999-03-23
 ; NUMBER OF SEQ ID NOS: 177
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 304
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: G1474
 US-10-278-173-30

Query Match 83.3%; Score 35; DB 4; Length 304;
 Best Local Similarity 87.5%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLQLRL 9
 ||||:|||
 Db 289 DLDLELRL 296

NUMBER: US 60/542,928
; PRIOR RESULT 2
US-11-435-388-836
; Sequence 836, Application US/11435388
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert A
; APPLICANT: RATCLIFFE, Oliver J
; APPLICANT: CANALES, Roger D
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; APPLICANT: MORRISON, Tracy A
; APPLICANT: KEDDIE, James S
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: CENTURY, Karen S
; APPLICANT: ADAM, Luc
; APPLICANT: ZHANG, James Z
; APPLICANT: HEMPEL, Frederick D
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS
; FILE REFERENCE: 514442005421
; CURRENT APPLICATION NUMBER: US/11/435,388
; CURRENT FILING DATE: 2006-05-15
; PRIOR APPLICATION NUMBER: WO PCT/US2004/037584
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/714,887
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/527,658
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: US 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/533,029
; PRIOR FILING DATE: 2000-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1018
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 836
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G359 polypeptide

US-11-435-388-836

Query Match 81.4%; Score 35; DB 7; Length 204;
Best Local Similarity 87.5%; Pred. No. 4.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLDLRL 9
||||:|
Db 194 DLDLRL 201

RESULT 7

S60325

transcription factor SUPERMAN - Arabidopsis thaliana

N;Alternate names: CCHH zinc finger protein

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 06-Sep-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C;Accession: S60325

R;Sakai, H.; Medrano, L.J.; Meyerowitz, E.M.

Nature 378, 199-203, 1995

A;Title: Role of SUPERMAN in maintaining Arabidopsis floral whorl boundaries.

A;Reference number: S60325; MUID:96069740; PMID:7477325

A;Accession: S60325

A;Molecule type: mRNA

A;Residues: 1-204 <SAK>

A;Cross-references: UNIPROT:Q38895; UNIPARC:UPI00000A019D; EMBL:U38946;

NID:g1079668; PIDN:AAC49116.1; PID:g1079669

A;Note: DNA sequencing was also done

C;Genetics:

A;Gene: SUP

C;Keywords: DNA binding; leucine zipper; nucleus; transcription factor;
transcription regulation; zinc finger

Query Match 81.4%; Score 35; DB 2; Length 204;

Best Local Similarity 87.5%; Pred. No. 20;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLRL 9

||||:|

Db 194 DLDLELRL 201

RESULT 8

T02540

probable C2H2-type zinc finger protein At2g37740 [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein F13M22.24

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C;Accession: T02540; E84796

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.

submitted to the EMBL Data Library, June 1998

A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.

A;Reference number: Z14677

A;Accession: T02540

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-304 <ROU>

A;Cross-references: UNIPROT:O80942; UNIPARC:UPI000000AB7CB; EMBL:AC004684;

NID:g3236234; PID:g3236256

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84796

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-304 <STO>

A;Cross-references: UNIPARC:UPI000000AB7CB; GB:AE002093; NID:g3236256;

PIDN:AAC23644.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g37740; F13M22.24

A;Map position: 2

Query Match 81.4%; Score 35; DB 2; Length 304;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLRL 9
|||:|
Db 289 DLDLRL 296

RESULT 2

T02540

probable C2H2-type zinc finger protein At2g37740 [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein F13M22.24

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C;Accession: T02540; E84796

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.

submitted to the EMBL Data Library, June 1998

A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.

A;Reference number: Z14677

A;Accession: T02540

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-304 <ROU>

A;Cross-references: UNIPROT:O80942; UNIPARC:UPI000000AB7CB; EMBL:AC004684;

NID:g3236234; PID:g3236256

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84796

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-304 <STO>

A;Cross-references: UNIPARC:UPI000000AB7CB; GB:AE002093; NID:g3236256;

PIDN:AAC23644.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g37740; F13M22.24

A;Map position: 2

Query Match 90.5%; Score 38; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLELRL 9
|||
Db 289 DLDLELRL 296

RESULT 10

US-10-412-699B-902

; Sequence 902, Application US/10412699B
; Publication No. US20040045049A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants

; FILE REFERENCE: MBI-0048CIP

; CURRENT APPLICATION NUMBER: US/10/412,699B

; CURRENT FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: 09/394,519

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: 09/489,376

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: 09/506,720

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 09/533,030

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,392

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,029

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/532,591

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,648

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/713,994

; PRIOR FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: 09/819,142

; PRIOR FILING DATE: 2001-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2011

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 902

; LENGTH: 304

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; FEATURE:

102e

; OTHER INFORMATION: G1474
US-10-412-699B-902

Query Match 90.5%; Score 38; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DLDLELRL 9
| | | | | | | |
Db 289 DLDLELRL 296

↑
NOT
NC:G1 031

RESULT 11

SUP_ARATH

ID SUP_ARATH STANDARD; PRT; 204 AA.
AC Q38895;
DT 09-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 47.
DE Transcriptional regulator SUPERMAN.
GN Name=SUP; Synonyms=FLO10; OrderedLocusNames=At3g23130;
GN ORFNames=K14B15.1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], FUNCTION, AND MUTANT SUP-3.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=96069740; PubMed=7477325; DOI=10.1038/378199a0;
RA Sakai H., Medrano L.J., Meyerowitz E.M.;
RT "Role of SUPERMAN in maintaining Arabidopsis floral whorl
RT boundaries."; ✓
RL Nature 378:199-203(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=20277480; PubMed=10819329; DOI=10.1093/dnares/7.2.131;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP FUNCTION, AND MUTANT FLO-10.
RC STRAIN=cv. Columbia;
RX PubMed=12324589; DOI=10.1105/tpc.3.11.1221;
RA Schultz E.A., Pickett F.B., Haughn G.W.;
RT "The FLO10 gene product regulates the expression domain of homeotic
RT genes AP3 and PI in Arabidopsis flowers.";
RL Plant Cell 3:1221-1237(1991).
RN [4]
RP FUNCTION, AND MUTANT SUP-1.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=92315906; PubMed=1352237;
RA Bowman J.L., Sakai H., Jack T., Weigel D., Mayer U., Meyerowitz E.M.;
RT "SUPERMAN, a regulator of floral homeotic genes in Arabidopsis.";
RL Development 114:599-615(1992).
RN [5]
RP FUNCTION, AND GENETIC REGULATION.
RX MEDLINE=20463033; PubMed=11006335; DOI=10.1105/tpc.12.9.1607;
RA Sakai H., Krizek B.A., Jacobsen S.E., Meyerowitz E.M.;
RT "Regulation of SUP expression identifies multiple regulators involved
RT in Arabidopsis floral meristem development.";
RL Plant Cell 12:1607-1618(2000).
RN [6]
RP FUNCTION, AND IDENTIFICATION OF THE CARBOXY-TERMINAL REPRESSION

RP DOMAIN.

RX MEDLINE=21940563; PubMed=11943180; DOI=10.1016/S0014-5793(02)02435-3;

RA Hiratsu K., Ohta M., Matsui K., Ohme-Takagi M.;

RT "The SUPERMAN protein is an active repressor whose carboxy-terminal

RT repression domain is required for the development of normal flowers.";

RL FEBS Lett. 514:351-354(2002).

RN [7]

RP INDUCTION.

RX MEDLINE=21930466; PubMed=11898023; DOI=10.1038/nature731;

RA Jackson J.P., Lindroth A.M., Cao X., Jacobsen S.E.;

RT "Control of CpNpG DNA methylation by the KRYPTONITE histone H3

RT methyltransferase.";

RL Nature 416:556-560(2002).

RN [8]

RP STRUCTURE BY NMR OF 41-79.

RX PubMed=12616630; DOI=10.1002/cbic.200390028;

RA Isernia C., Bucci E., Leone M., Zaccaro L., Di Lello P., Digilio G.,

RA Esposito S., Saviano M., Di Blasio B., Pedone C., Pedone P.V.,

RA Fattorusso R.;

RT "NMR structure of the single QALGGH zinc finger domain from the

RT Arabidopsis thaliana SUPERMAN protein.";

RL ChemBioChem 4:171-180(2003).

CC -!- FUNCTION: Probable transcriptional regulator considered as

CC cadastral protein that acts indirectly to prevent the B class

CC homeotic proteins APETALA3 and perhaps PISTILLATA from acting in

CC the gynoeical whorl. Principal function is to balance cell

CC proliferation in the third and fourth whorls of developing flowers

CC thereby maintaining the boundary between stamens and carpels. May

CC fulfill this role by repressing genes implicated in cell division.

CC Plays equally a role in the determinacy of the floral meristem. Is

CC also required for normal ovule development.

CC -!- SUBCELLULAR LOCATION: Nucleus.

CC -!- TISSUE SPECIFICITY: Expressed early in the third whorl, and later

CC becomes localized at the boundary between the stamen and carpel

CC whorls. Also detected in developing ovule primordia.

CC -!- INDUCTION: Repressed by KRYPTONITE/SUVH4, member of the histone

CC H3-K9 methyltransferase family that contributes with other factors

CC to the CpNpG methylation of the SUP gene resulting in its

CC silencing. The alternative epigenetic states of the SUPERMAN locus

CC have been called Clark Kent alleles. Positively regulated at an

CC early stage of development by LEAFY and by B class homeotic

CC proteins APETALA3 and PISTILLATA. Later expression is maintained

CC by both the B class homeotic proteins and the C class homeotic

CC protein AGAMOUS. These two steps of regulation require the

CC intervention of additional factors.

CC -!- DOMAIN: Contains two overlapping leucine-zipper-like motifs at the

CC C-terminal region, which might serve as a site for protein-protein

CC interaction. In this domain, a slightly degenerated ERF-associated

CC amphiphilic repression (EAR) motif seems to be involved in the

CC activity of transcriptional repression.

CC -!- MISCELLANEOUS: Mutations in SUP cause the ectopic expression of

CC APETALA3 leading to the development of extra stamens at the

CC expense of the central carpels of the flower.

CC -!- SIMILARITY: Contains 1 C2H2-type zinc finger.

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

```

CC -----
DR EMBL; U38946; AAC49116.1; -; Genomic_DNA.
DR EMBL; AB025608; BAA95724.1; -; Genomic_DNA.
DR PIR; S60325; S60325.
DR PDB; 1NJQ; NMR; A=42-78.
DR TRANSFAC; T02275; -.
DR GenomeReviews; BA000014_GR; AT3G23130.
DR TAIR; At3g23130; -.
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW 3D-structure; Developmental protein; Differentiation; DNA-binding;
KW Flowering; Metal-binding; Nuclear protein; Repressor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT CHAIN      1      204      Transcriptional regulator SUPERMAN.
FT                                     /FTid=PRO_0000047839.
FT DOMAIN     153     204      Leucine-zipper-like.
FT ZN_FING     47      69      C2H2-type.
FT MOTIF      195     199      EAR-like (transcriptional repression).
FT MUTAGEN     63      63      G->D: In sup-3.
FT STRAND     44      48
FT TURN       50      52
FT STRAND     55      58
FT HELIX      59      67
FT TURN       68      69
FT STRAND     72      72
FT TURN       74      77
SQ SEQUENCE   204 AA;  23084 MW;  2CF36E29A821F76E CRC64;

```

```

Query Match          83.3%;  Score 35;  DB 1;  Length 204;
Best Local Similarity 87.5%;  Pred. No. 76;
Matches      7;  Conservative    1;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 DLDLQLRL 9
        ||||:|||
Db     194 DLDLELRL 201

```